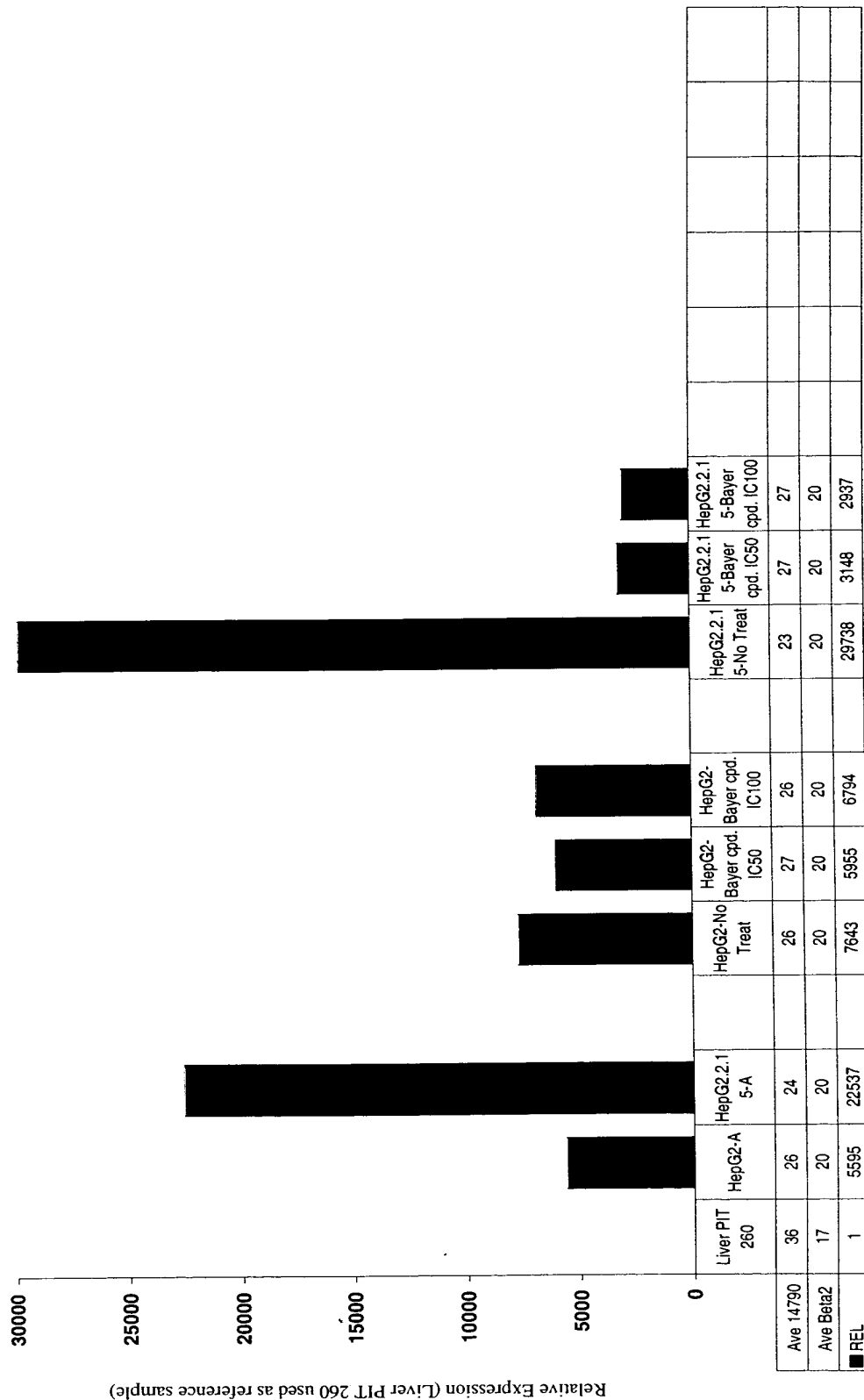


Ser/thr Kinase 14790 Expression on HBV+ Liver



14790HepG2.2.15

14790 Expression on HepG2.2.15 (HBV-expressing cell line)



Gene 14790 Expression in Normal Human Tissue Relative Expression (Thyroid as Reference)

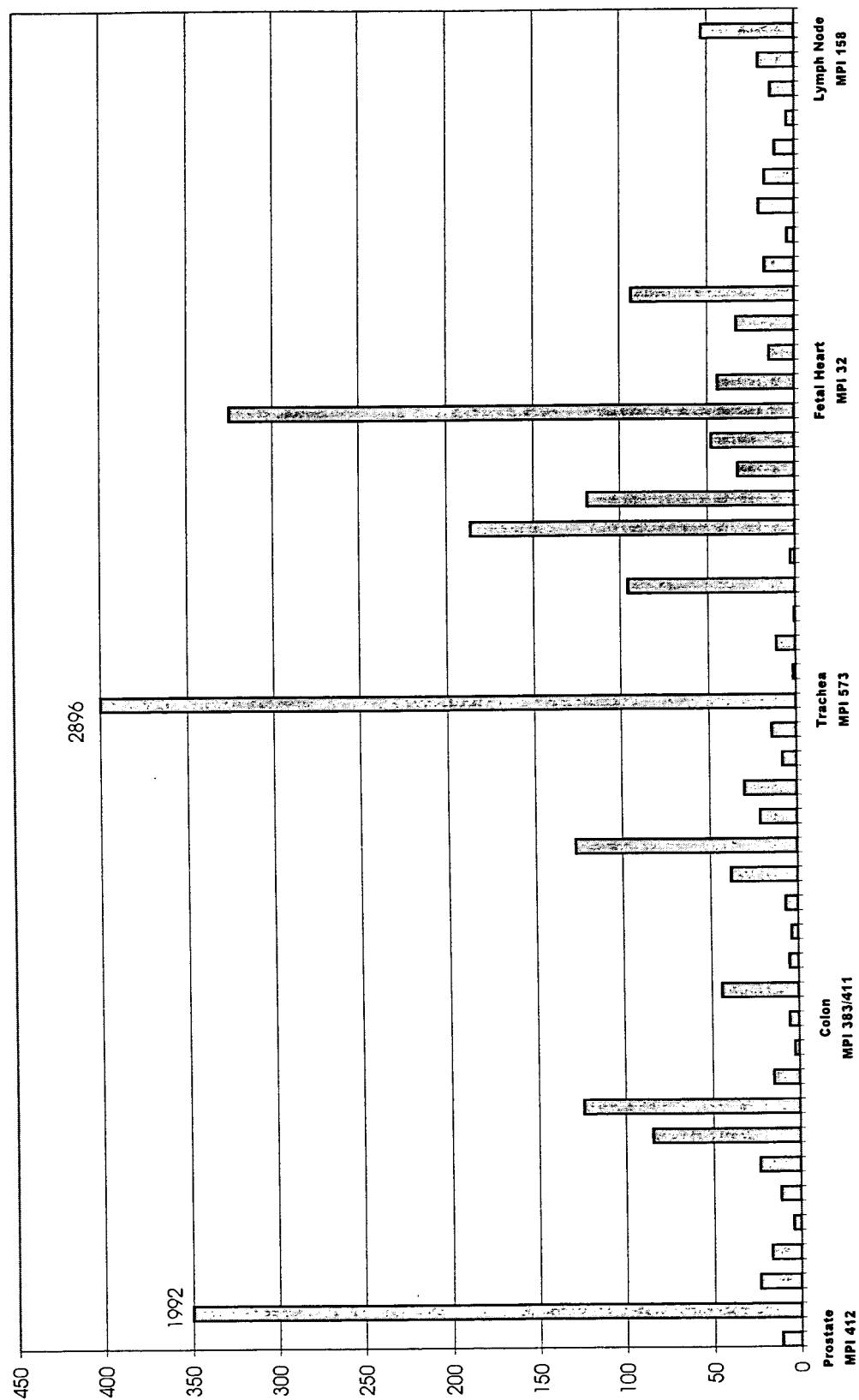


FIG. 5

Thursday, February 3, 2000 4:20 PM

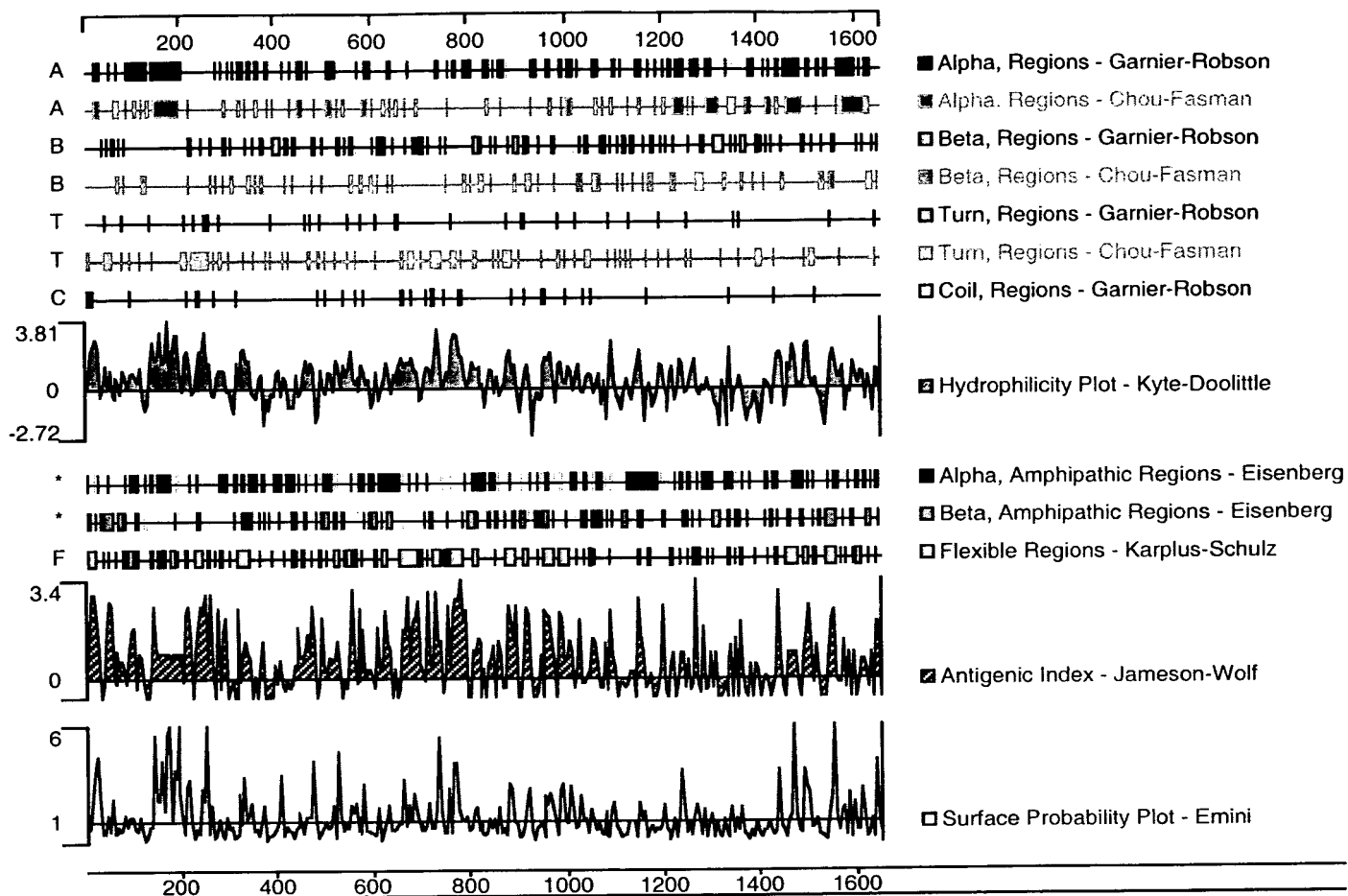
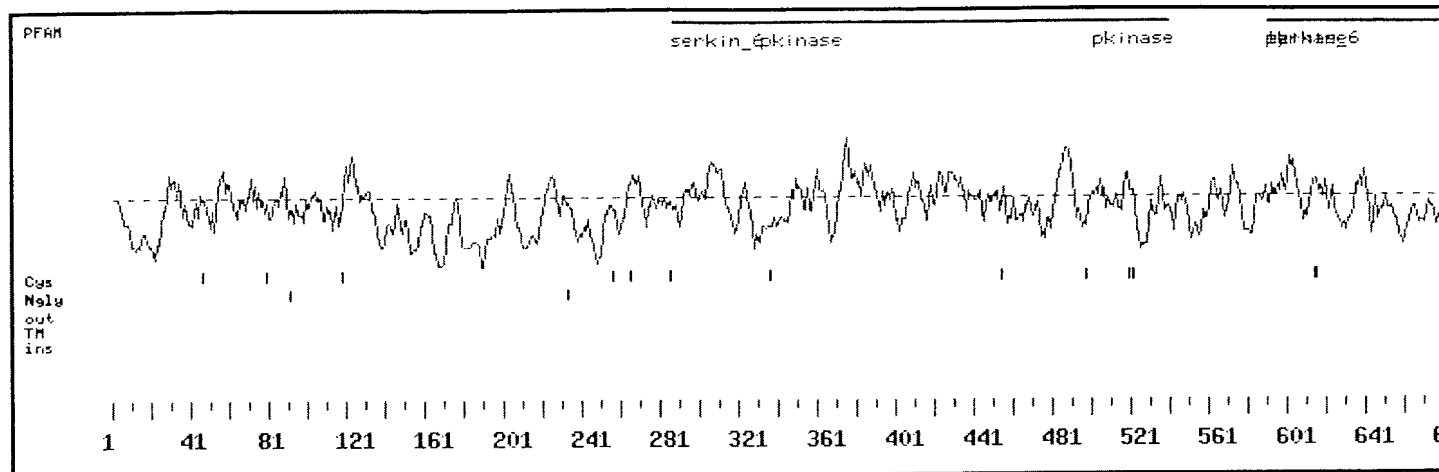


FIG. 6

[Back to orfanal.cgi](#)

Analysis of 14790 (1649 aa)



>14790
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDAGCPVKEPPEINLVLY
PQGLTGEEVYVVDLVRVKCPPTYPDVPEIELKNAKGLSNESVNLKSRLEELAKKHCGE
VRIFFELAYHVQSFLEHNKPPPKSFHEEMLEERRAQEEQORLLEAKRKEEQEQRILHEIQ
PKKEEIKKEKKRKEMAKQERLEIASLSNQDHTSKKDPGCHRTAAIHLGGSPDFVNGKHR
ASSGRSRRRERYVCSNSEDSPGSCILYFNMGSPDQLMVHGKCKIGSDQGLKLVYNAL
FEATGGFVLLYEWVLQWQKMGPFLLTSQEKEKIDCKKKQIQGTETEFNSLVKLSHPNVVR
KLAMNLKEQDDSIIVVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLHSNS
VYHKVLSASNVLDVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSNALPYKTGKKGD
VRLGLLLLSLQSGQEGCEYPTIPSDLPADFDQFLKKCVCLDDKERWSPQQLKHSFIN
QPKMPLVQSPEDSGGQDYVETVIPSNNRLPSAAPPSETQRFQSRFYIEFEELQLLGKGA
FEAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLISRLHHEINIVRYNAWIERHE
RAGPGTPPPDSGLAKDDRAARQGPASDITDGLDSVEAAAPPILSSSVWSTSGERSAS
RFPATGPGSSDDEDDDEHGGVFSQSFLPASDSSEDIIFDNEDENSKSQNQDEDCNEK
MGCHSESPVTTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
EKGMIHRDLKPVNIFLSDDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG
VGTALYVSPEVQGSTKSAYNQKVDLFLSLGIIFFEMSYHPMVTASERIFVLNQLRDPSTP
KFPEDFDGGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPQMESESELHEVLHHTLT
VYDGKAYRTMAQIFSQRISPAIDYTDSDILKGNFSIRTAKMQQHVCEIIRIFKRHGA
VLCPTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNILNLKRYCIE
RFRPRKLDRFHPKELLECAFDIVTSTNSFLPTAEIITYIIEFFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTREVEAKFCNLSLSSNSLCRLYKF
EQQKGLQDLMPNTINSLIKQKTGIAQLVKYGLKDLSEVVGLLKKLGIKLQVLINLGLVYK
VQOHNGIIPQFVAFIKRRQRAVPEILAAAGGRYDILLIPQFRGPOALGPVPTAIGVSIADK
TAAVLNMEESVTISSCDLLVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVVKVSFEKERQTEKRVLETVDHVLQKLRTKVTDERNG
READSNLAVQNLKGSFNASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSEIELAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYRILF

PSORT Prediction of Protein Localization

MITDISC: discrimination of mitochondrial targeting seq

R content: 3 Hyd Moment(75): 7.37
Hyd Moment(95): 6.02 G content: 5
D/E content: 2 S/T content: 0
Score: -6.53

Gavel: prediction of cleavage sites for mitochondrial preseq

R-2 motif at 20 GRG|RD

NUCDISC: discrimination of nuclear localization signals

pat4: KRRK (5) at 190
pat4: RPRK (4) at 1144
pat7: none
bipartite: RRAQEEQORLLEAKRKE at 152
bipartite: KRIPINPASRQFRRIKG at 619
content of basic residues: 12.1%
NLS Score: 1.08

ER Membrane Retention Signals:

FIG. 7a

<http://tango.mpi.com/seqanal/orfanal/14790.16890.html>

XXRR-like motif in the N-terminus: AGGR

none

Final Results (k = 9/23):

56.5 %: nuclear
30.4 %: cytoplasmic
4.3 %: vacuolar
4.3 %: mitochondrial
4.3 %: vesicles of secretory system

prediction for 14790 is **nuc** (k=23)

Start	End	Feature	Seq
144	204	coiled coil	FHEEMLERRA...AKQERLEIAS

Signal Peptide Predictions for 14790

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
1522	1538	ins-->out	0.8

14790
MGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACPVPKPEPEINLVLY
PGLTGEEVYVKVLDLRVKCPPTYPDVVEPEIELKNAKGLSNESVNLLKSRLLEELAKKHCGE
VIFELAYHVQSFLEHNKPPPKSFHEEMLERRAQEEQORLLEAKRKEEQREILHEIQ
EKEEIKKEKKRREMAKQERLEIASLSNQDHTSKKDPGGHRTAAAILHGGSPDFVGNKGR
ANSSGRSRRRERQYVVCNSEDSPGSCILYFNMGS PDQLMVHKGKICIGSDEQLGKLVYNAL
TATGGFVLLYEWVLQWQKKMGPFLLTSQEKEKIDCKKKIQGTETEFNSLVKLSHPNVVR
FLAMNLKEQDDSI VVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLHSNS
VHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
MRLGLLLLSLSQGECEGYPTIPSDLPADFQDLKKCVCLDDKERWSPQQLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPSRLPSAAFFSETQRFQFSRYFIEFEELQLLGKGA
FAVIKQVKNLKGCCYAVKRIPINPASRQFRRIKGEVTLRLHHEINIVRYNNAWIERHE
PAGPGTTPPPDSGLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVWSTSGERSAS
ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSEDIIFDNEDENSKSNQDEDCNEK
WCHSESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
FRGMIHRDLKPVNIFLSDSDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG
MVG TALYVSPVQGSTKSAYNQKVDLFLSLGIFFEMSYPHMTASERIFVLNQLRDPSTP
KFPEDFDGGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPMEESELHEVLHHTLT
NVDGKAYRTNMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCTIIRIFKRHGA
VOLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNLNLKRYCIE
RVFRPRKLRDRFHPKELLECAFDIVTSTNSFLPTAEIITYIYIIEQFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTREVEAKFCNLSNSNLCRLYKF
IEQKGLDLQDMPTINSLIKQKTGIAQLVKYGLKDLLEVVGLLKKLGKQLVLINLGLVYK
VQQHNGIIFQFVAFIKRRQRAVPEILAGGRYDLLIPQFRGPQALGPVPTAIGVSIADK
ISAAVLNMEESVTISSCDLLVSVGQMSMRINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVVKVSFEKERQTEKRVLETELVDHVLQKLRKVTDERNG
READNLAVQNLKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSIEILAVDLPKETILQFLSLEWDAEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVFLYSYRDDYYRILF

Prosites Pattern Matches for 14790

Prosite version: Release 12.2 of February 1995

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 100 NESV 103

Query: 242 NSSG 245

<http://tango.mpi.com/seqanal/orfanal/14790.16890.html>

FIG. 7b

Query: 1055 NFSI 1058
Query: 1195 NYSI 1198
Query: 1201 NHTM 1204
Query: 1246 NLSL 1249
Query: 1414 NLTO 1417
Query: 1518 NASG 1521
Query: 1600 NTTV 1603

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE CAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 403 RRYT 406
Query: 988 KRPT 991
Query: 1630 KKVS 1633

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 212 TSK 214
Query: 244 SGR 246
Query: 247 SRR 249
Query: 438 TVK 440
Query: 447 SKR 449
Query: 475 TGK 477
Query: 567 SNR 569
Query: 579 TQR 581
Query: 720 SAR 722
Query: 809 TLR 811
Query: 822 TVR 824
Query: 915 STK 917
Query: 945 SER 947
Query: 959 SPK 961
Query: 1036 SQR 1038
Query: 1057 SIR 1059
Query: 1060 TAK 1062
Query: 1232 TEK 1234
Query: 1236 TRR 1238
Query: 1416 TQK 1418
Query: 1455 SDK 1457
Query: 1473 TEK 1475
Query: 1545 STR 1547
Query: 1602 TVK 1604
Query: 1639 SYR 1641

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 65 TGEE 68

FIG. 7e

Query: 82	TYPD	85
Query: 108	SRLE	111
Query: 144	SFHE	147
Query: 207	SNQD	210
Query: 213	SKKD	216
Query: 247	SRRE	250
Query: 326	TSQE	329
Query: 343	TETE	346
Query: 411	SGLD	414
Query: 551	SPED	554
Query: 688	SDTD	691
Query: 707	SSVE	710
Query: 713	TSGE	716
Query: 730	SSDD	733
Query: 753	SDSE	756
Query: 809	TLRD	812
Query: 880	SKQD	883
Query: 943	TASE	946
Query: 991	TATE	994
Query: 1020	TNVD	1023
Query: 1180	TIYE	1183
Query: 1236	TRRE	1239
Query: 1395	SSCD	1398
Query: 1435	SQEE	1438
Query: 1455	SDKE	1458
Query: 1570	SEIE	1573
Query: 1639	SYRD	1642

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 246	RSRRERQY	253
Query: 811	RDTIDQGLY	819
Query: 830	REILDGLAY	838
Query: 1444	RHHEITY	1450
Query: 1617	KLVCDEIY	1624

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 218	GGHRTA	223
Query: 384	GVSLAA	389
Query: 494	GQECGE	499
Query: 599	GAFGAV	604
Query: 613	GCCYAV	618
Query: 684	GQPASD	689

FIG. 7f

Query: 742 GGVFSQ 747
 Query: 782 GCHESE 787
 Query: 900 GMVGTA 905
 Query: 914 GSTKSA 919
 Query: 1373 GVSIAI 1378
 Query: 1514 GSFSNA 1519

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 475 TGKK 478

>PS00107|PDOC00100|PROTEIN_KINASE_ATP Protein kinases ATP-binding region signature.

Query: 596 LGKGAFGAV 604

>PS00108|PDOC00100|PROTEIN_KINASE_ST Serine/Threonine protein kinases active-site signature.

Query: 844 MIHRDLKPVNIFL 856

>PS00116|PDOC00107|DNA_POLYMERASE_B DNA polymerase family B signature.

Query: 687 ASDTDGLDS 695

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).
 HMM file: /prod/ddm/seqanal/PFAM/pfam4.4/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.16895.seq

Query: 14790

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
pkinaase	Eukaryotic protein kinase domain	282.0	7.8e-81	4
Ribosomal_L23	Ribosomal protein L23	5.0	3.9	1
mRNA_cap_enzyme	mRNA capping enzyme	-181.3	9.6	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
pkinaase	1/4	332	443	30	134	69.4	3.7e-18
pkinaase	2/4	501	539	237	278	22.8	3.2e-05
pkinaase	3/4	590	662	1	66	51.2	4.2e-13
pkinaase	4/4	797	1001	65	278	138.7	1.1e-37
Ribosomal_L23	1/1	1223	1244	1	23	5.0	3.9
mRNA_cap_enzyme	1/1	1004	1309	1	504	-181.3	9.6

Alignments of top-scoring domains:

pkinaase: domain 1 of 4, from 332 to 443: score 69.4, E = 3.7e-18
 *->ilk..kesls..lrEiqilkrllsHpNivrlvgvfed...tddhlylv
 14790 332 KIDKCKKQIQgtETEFNSLVKLSHPNVVRYLAMNLKeqgDSIVVDIL 378
 mEymegGdLfdylrrngplsekeakkialQilrGleYlHsngivHRDLKp
 E+ g +L+ +l+ gp++ ++++++ Q+l+Gl+YlHsn++vH L +
 14790 379 VEHISGVSLAAHLSHSGPIPvHQLRRYTAQLLSGLDYLSNSVVKVLSA 428
 eNIlldengtVKiaD<-*
 +N+L+d +gtvKi+D
 14790 429 SNVLVDAEGTVKITD 443

<http://tango.mpi.com/seqanal/orfanal/14790.16890.html>

FIG. 7g

pkinese: domain 2 of 4, from 501 to 539: score 22.8, E = 3.2e-05

```
*->rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<-*
+ +ps ++ +dd+lkkc ++D ++R+ + +l+h +
14790 501 PVTIPSDLPADFQDFLKKCVCLDDKERW---SPQQLKHFSFI 539
```

pkinese: domain 3 of 4, from 590 to 662: score 51.2, E = 4.2e-13

```
*->yelleklGeGsfGkVykakhk.tgkivAvKilkesls.....lrE
+e l+ lG+G+fG V k+++k +g+ +AvK ++ s++ ++ E
14790 590 FEELQLLGKGAFGAVIKVQNKIDGCCYAVKRIPINPASrqfrrikGE 636
```

```
iqilkrslshpNivrllgvfedtdhdl<-*
+ +l rl+h+Niv++ ++ ++++++
14790 637 VTLLSRLHHENIVRYNAWIERHERP 662
```

pkinese: domain 4 of 4, from 797 to 1001: score 138.7, E = 1.1e-37

```
*->hlylvmEymegGdLfdylrrngplsekeakkialQilrGleYlHsng
+ly+ mEy+e+ L+d + + + + +++++il Gl+Y+H++g
14790 797 YLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIHEKG 843
```

```
ivHRDLKpeNILdengtvKiadFGLArll.....
+HRDLKp NI+ld++ +vKi+DFGLA++ + ++++++++ +
14790 844 MIHRDLKPVNIIFLSDDHVKIGDFGLATDHLafsadskqddqtdgliksd 893
```

```
..ekltttfGTpWymmAPEvileg...rgysskvDvWSlGvilyElitgg
++++lt+ vGT Y+ +PEV +g++++ y kvD SlG+i++E+
14790 894 psGHLTGMVGTALYV-SPEV--QGstkSAYNQKVDLFSGLIIFEMS--- 937
```

```
plfpgadlpftggdevdqliifvklPfsdelpktridpleelfrikkr
P e++f +++
14790 938 -----YHPMV-----TASERIFVLNQL 954
```

```
....rlplpsncSee....lkdLlkkcLnkDPskRpGsatakeilnhpwf
++++ ++p+ + + + + k+++++Ln DP+kRp ta+e+l++ +
14790 955 rdptSPKPFEDFDDGehakQKSVISWLLNHDPAKRP---TATELLKSELL 1001
```

```
<-*
14790 - -
```

Ribosomal_L23: domain 1 of 1, from 1223 to 1244: score 5.0, E = 3.9

```
*->tdiikyPviTeKlamnlleepNk<-*
+ii y +TeKl++++e ++
14790 1223 VYIILYDAVTEKLTRREVEA-KF 1244
```

mRNA_cap_enzyme: domain 1 of 1, from 1004 to 1309: score -181.3, E = 9.6

```
*->nqtteRvyelhkiElfsvpelngKKiglgikLpkttdteslrmVakl
q++e + e+ l L++d++ rtm a+
14790 1004 PQMEES-----ELHEV-----LHHTLTNVGDKAYRTMMAQI 1034
```

```
lglamktktfPddeGsqPVsferkdleesLkekdyfveceKTDGircshgF
+ P + + + + + vce ir+
14790 1035 FS----QRISPAIDYTYDSILKGNFSIRTAKMQQHVCETI--IRI--- 1074
```

```
NRTGFLIAAaLlFlvehpgleeaiSHiLSgef..lidReknyYKQDYIDl1
+ h + + + l+ R +Y ++
14790 1075 -----FKRHGAVQL-----CTPlLLPRNRQIY-----EHN 1099
```

```
pkr1fPrekdktkakelpthyrgtllDGEIvidinriaveqkTlrYvFD
++ lf + + l++ l d ++ rYv +
14790 1100 EAALFMD-----HSGMLVM-LPFD----LRIPF-ARYVARN 1129
```

```
alaisGqtviqrd.lskrlgdefikavkKpfdefkkvmpdakilnqqkYN
+ ++ + i+r + L+ f +e+ d+++++
14790 1130 NILNLKRYCIERVFPRKLDLDR-F-----HPKELLECAFDIVTSTT--- 1168
```

```
FpfkiglkhsmslygqlklkaeskmviskadampkllHinDGLiftcivr
f++ + ++y ++ + a +
14790 1169 NSFLPTAEIITYIYIEIIEFPA-----L-----QE- 1193
```

```
dtpyieGeilVEPGNSYlDfnLlKWKpkeenTvDFelilefeevndPeld
++++i+ + Llk +l + +
14790 1194 RNYSIYL-----NHTMLLKA-----ILLHCG-----IP 1216
```

```
ekdgfslyLdYdampGELfkfslgVWqgGfnkrFevihtdqiffrvafqk
e++ + + + + + + + + + + +
14790 1217 EDK-----LSQVYIILY-DAVTEKLTRRE-----VEAK- 1243
```

```
lgRlkhefaelsVsdkdwyklkaleqpldGrIVEcrladieilIFQegrw
f +ls+s +l + +E ++ +
14790 1244 -----FCNLSSLSSNSLCRLY-----KFIEQKGLQD----- 1269
```

```
eylrfRdDKqgalKtgGYsgNhistvekvllsikDgvsieElklfpGmY
+ ++ + q+ tg + + + + + kD +E+ l
```

<http://tango.mpi.com/seqanal/orfanal/14790.16890.html>

FIG. 7h

14790 1270 LMPTINSLIKQK--TG-----IAQLVKYGLKD---LEEVVGLLK--- 1303

FAGAktlikr<-*

k +ik

14790 1304 ----KLGIKL 1309

//

Searching for complete domains in SMART

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine

HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /ddm/robison/smart/smart/smart.all.hmms

Sequence file: /prod/ddm/wspace/orfanal/oa-script.16895.seq

Query: 14790

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
serkin_6		184.2	2.2e-51	2
tyrkin_6		-40.3	2e-09	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
serkin_6	1/2	286	539 ..	1	231 {}	17.2	2.2e-11
serkin_6	2/2	590	1001 ..	1	231 {}	166.8	3.5e-46
tyrkin_6	1/1	590	1001 ..	1	280 {}	-40.3	2e-09

Alignments of top-scoring domains:

serkin_6: domain 1 of 2, from 286 to 539: score 17.2, E = 2.2e-11

```

*->YellkkkIGkGAFGkVylardkktgrlvAiKvik.....
      ++lGK      Vy a ++ tg v  + + + + +
14790 286  IGSDEQLGK----LVYNALETATGGFV---LLYewvlqwqkkmqpf1 325

.....erilrEikiLkk.dHPNIVkLydvfed....dkl
+++++++ + + + + + + + E + L k HPN+V+++ + + + + +
14790 326  tsqekidkckkqiQGTETEFNSLVK1SHPNVVRYLAMNLKegddsIVV 375

ylVmEyceGdlGdLfdllkkrgrgrlrvlE.earfyfrQilsaLeYlH
+ E+++G +L +l + g+ + + + r+y++Q+ls+L+YlH
14790 376  DILVEHISG--VSLAAHLSHSGP-----IPVhQLRRYTAQLLSGLDYlH 417

sqqIiHRDLKPeNiLLds..hvKladFGLArql.....ttfvGTp
s+ ++H L +N+L+d ++vK++D ++++l + + + + t v
14790 418  SNSVVHVLSASNVLVDAegTVKITDYSISKRLadickedvfeQTRV--- 464

eYmAPEv1.....gYgkpavDiWslGcilyEl1tGkpPfpqldlifkk
++++ + + gk + D+W lG +l l G+ + + +
14790 465  -----RFsdnalpyKTGK-KGDVWRLGLLLLLSLQQQE-----CGEYPV 502

ig....SpeakdLikkLlvkdPekRlta.eaLedeldikaHPff<-*
+++ + + d++kk+ + d ++R++ ++L+ H f+
14790 503  TIpsdlPADFQDFLKKCVCLDDKERWSPqQLK-----HSFI 539

```

serkin_6: domain 2 of 2, from 590 to 1001: score 166.8, E = 3.5e-46

```

*->YellkkkIGkGAFGkVylardkktgrlvAiKvik.....
+e l++lGkGAFG V +++++ +g +A+K+i+ + + + + +
14790 590  FEELQLLGKGAFAVAVIKVQNKLDGCCYAVKRIPinpasrqfrrikge 636

.....
+ + + + + + + + + + + + + + + + + + + + +
14790 637  vtllsrhhenivryynawierherpagpgtpppsgplakddraargqp 686

.....
+++++ + + + + + + + + + + + + + + + + + + + +
14790 687  asdtgdldsvaaappilsssvewstsgersasarfpatgpgssddedd 736

.....erilrEikiLkk...dHPNIVkLydv
+++++++ + + + + + + + + + E + + + + + + + + +
14790 737  dedehgfvfsqsf1pasdsesdiiFDNEDENSKSQNqdeDCNEKNGCHES 786

fed.....dklylVmEyceGdlGdLfdllkkrgrgrlrvlE.earfy
+ + + + +ly+ mEyce +L+d + + + + + + + + +
14790 787  EPSvtteavHYLYIQMEYCEK--STLRDTIDQGLY-----RDTvRLWRL 828

frQilsaLeYlHsqqIiHRDLKPeNiLLds..hvKladFGLArql....
fr+il++L+Y+H++g iHRDLKP Ni+Lds++hvK++DFGLA+ +
14790 829  FREILDGLAYIHEKGMiHRDLKPVNIFLDSddhVKIGDFGLATDh1afsa 878

.....ttfvGTpeYmAPEv1.....gYgkpavDiW
+++++++ + + + + + + + + + + + + + + + + + + + + +

```

FIG. 7i

<http://tango.mpi.com/seqanal/orfanal/14790.16890.html>

```

14790 879 dskqddqtdgliksdpsghltGMVGTALYVSPEVQgstksAYNQ-KVDLF 927
      SlGcilyElltGkpPFp..qldlifkkig.....Speakd
      SlG+i++E+ + p ++ ++++++++ + + + + + k+
14790 928 SLGIIFFEMS-HPMVTasERIFVLNQLRdptspkfpddgeHAKQKS 976
      LikklLvkdPekRlta.eaLedeldikaHPff<-*
      i+ lL+ dP+kR+ta+e+L+ + +
14790 977 VISWLLNHDPakRPTAtELLK-----SELL 1001

tyrkin_6: domain 1 of 1, from 590 to 1001: score -40.3, E = 2e-09
*->ltlgkklGeGaFGeVykGtlk...ieVAVKtLkeda....keeFlrE
+ ++ LG GaFG V k + k ++ AVK + + + + + E
14790 590 FEELQLLGKGAFGAVIKVQNkldgCCYAVKRIPINPasrqFRRIKGE 636
      akiMkklGgkHpNiVklLgVcteeerrFmevePlmivmEymegGdLldyL
      +++++ +H+NiV+ + + +e
14790 637 VTLLSRL--HHENIVRYNAWIE----- 657
      rknrpK.....
      r rp ++++++++ + + + + + + + + + + + + + + + + +
14790 658 RHERPAGpgtpppdsqplakddraargqpasdtdgldsveaaapppiLs 707
      + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
14790 708 svewstsgersasarfpatgpgssdddeddehgvgfsqsfldpsdses 757
      + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
14790 758 diifdnedensksqngdedcnekngcheseptteavhyliqmecek 807
      .....lsldLlsfAlQIAkGMeYLesknfvHRDLAARNcLvG
      ++ + + + + + L I +G +Y+++k+ +HRDL N+ ++
14790 808 stlrtdidqglyRDTVRLWRLFREILDGLAYIHEKGMiHRDLKPVNIFLD 857
      enkvvKisDFGLsRdlyddDkkG....eskdYrkkkggkgtllPir.
      ++ +VKI+DFGL+ d+ ++ +++++ +d + + + + + + + + +
14790 858 SDDHVKIGDFGLATDHLAF-SADskqddQTGDLIKSDPSGHLTGMVGTAL 906
      WmAPesl..kdgkFtskSDVWSFGVlLWEiftlGeqPYpgeiqqfmsnee
      +PE+ ++ + + + k D +S G+ +E+ Y + + + + +
14790 907 YVSPEVQgsTKSAYNQKVDLFSLGIIFEM-----SYHPM---VTASE 946
      ...vleylkkGyRlpkPendlpisS.vtCPdelYdlmlqCwaedPedRPt
      + vl++l++ ++ Pe+ ++ + + + + + + + + + + + + + + + + + + + + +
14790 947 rifVLNQLRDPtSPKFPED-----FdDGEHAKQKSVISWLLNHDPakRPT 991
      Fsel..verl<-*
      +el + e+l
14790 992 ATElKSELL 1001

```

ProDom Matches

FIG. 7j

ProdomId	Start	End	Description	Score
View Prodom 40346 <input type="button" value="Boxer"/> <input type="button" value="Showing match"/> <input type="button" value="Go!"/>	18	323	p99.2 (2) O01712(1) O61651(1) // INITIATION FACTOR KINASE EUKARYOTIC EIF-2 ALPHA EIF-2ALPHA	295
View Prodom 137719 <input type="button" value="Boxer"/> <input type="button" value="Showing match"/> <input type="button" value="Go!"/>	19	1504	p99.2 (1) O74297_NEUCR // CPC3 PROTEIN	87
View Prodom 1 <input type="button" value="Boxer"/> <input type="button" value="Showing match"/> <input type="button" value="Go!"/>	341	1017	p99.2 (2773) CC2(14) KKIT(14) KPC1(13) // KINASE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE-PROTEIN PHOSPHORYLATION RECEPTOR TYROSINE-PROTEIN PRECURSOR TRANSMEMBRANE	107
View Prodom 150228 <input type="button" value="Boxer"/> <input type="button" value="Showing match"/> <input type="button" value="Go!"/>	1105	1206	p99.2 (1) O74297_NEUCR // CPC3 PROTEIN	90
View Prodom 2305 <input type="button" value="Boxer"/> <input type="button" value="Showing match"/> <input type="button" value="Go!"/>	1106	1230	p99.2 (23) SYH(12) // SYNTHETASE AMINOACYL-TRNA HISTIDYL-TRNA PROTEIN LIGASE ATP-BINDING BIOSYNTHESIS HISTIDINE--TRNA HISRS KINASE	137
View Prodom 42726 <input type="button" value="Boxer"/> <input type="button" value="Showing match"/> <input type="button" value="Go!"/>	1274	1648	p99.2 (2) O01712(1) O61651(1) // INITIATION FACTOR KINASE EUKARYOTIC EIF-2 ALPHA EIF-2ALPHA	221
ProdomId	Start	End	Description	Score

View Prodom 40346

40346 p99.2 (2) O01712(1) O61651(1) // INITIATION FACTOR KINASE EUKARYOTIC
EIF-2 ALPHA EIF-2ALPHA
Length = 296

Score = 295 (108.9 bits), Expect = 1.7e-28, Sum P(2) = 1.7e-28
Identities = 58/144 (40%), Positives = 95/144 (65%)

Query: 18 SYPQRQDHELQALEAIYGADFQDLRPDAGPVPKEPPEINLVLYP--QGLTGEEVYVKVDL 75
S+ +RQ EL+ +++I+G D +DLRP A + +P +I + L P G E YV L
Sbjct: 9 SFRERQAQELEVIKSIIFGCDVEDLRPQANPSLWKPTDIRIQLTPLRDSSNGLETYVCTKL 68

Query: 76 RVKCPPTYPDVVPEIELKNAKGLSNESVNLKSRLEELAKKHCGEVMIFELAYHVQSFLS 135
V CP YP + P+I L+ +KG+S++ + L+++L+ +++ GEVMI+ELA VQ+FL
Sbjct: 69 HVTCPSPKYPKLPKISLEESKGMSDQLLEALRNQLQAQSQELRGEVMYELAQTVAFL 128

Query: 136 EHNKPPPKSFHEEMLERRAQEEQQ 159
EHNKPP SF+++ML+ + + +Q+
Sbjct: 129 EHNKPPKGSFYDQMLQDKQKRDQE 152

Score = 63 (27.2 bits), Expect = 1.7e-28, Sum P(2) = 1.7e-28
Identities = 15/59 (25%), Positives = 30/59 (50%)

Query: 266 EILYFN-MGSPDQLMVHKGKIGSDEQLGLVYNALETATGGFVLLYEWVLQWQKKMGF 323
E LYF+ MG + +G C+G ++ G + Y ++ G + + EW +++ + P
Sbjct: 230 ETLYFHKMGR----QIQRGCCVGHSSQR-GCIAYTGIDMHCGQLLYITEWNIKYSQLEQP 283

View Prodom 42726

>42726 p99.2 (2) O01712(1) O61651(1) // INITIATION FACTOR KINASE EUKARYOTIC
EIF-2 ALPHA EIF-2ALPHA
Length = 469

Score = 221 (82.9 bits), Expect = 7.5e-15, P = 7.5e-15
Identities = 92/341 (26%), Positives = 160/341 (46%)

FIG. 7k

Query: 1274 INSLIKQKGTGIAQLVKYGLKDLEEXXXXXXXXXXXXXXXXXNLGLVYKQQ--HNGIIFQF 1331
+ SL++ K A L + L++LE GL + + GI++Q
Sbjct: 70 LKSLMRGKGEAASLARGALRELETVVGLAYSLGVKCPHIWAGLPISFDRASNGGIVWQM 129

Query: 1332 VAFIKRRQRAVPEILAAGGRYDLLIPQF-RGPQALGPVPTAIGV-----SIAIDKISAA 1384
A +K + P +LA G RYD ++ +F + Q P A GV + ++DK+ AA
Sbjct: 130 TADLKPNRSGHPSVLAIGERYDSMLHEFQKQAQKFNAMPARGVLSGAGLTFSLDKLVAA 189

Query: 1385 VLNMEESVTISSCDLLVSVGQMSMSRAINLTQKL-WTAGITAEIMYDWSQSQEELQEYC 1443
V +E + + D+ + G + + +L W+ GI I+ S+ +E Q+
Sbjct: 190 V-GVEYAKDCRAIDVGICVCGTRPPLKDVYIMRLLWSVGIRCGIVEAASELGDEAQLA 248

Query: 1444 RHHEITYVALVSDKEGSHVKVSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNGREA 1503
R + +V LV++ GS ++V+SFE+ER E+ + TELV+ + + LR+ D NG
Sbjct: 249 RLQAL-HVILVAEN-GS-LRVRSFERERFQERHLTRTELVEFIQKMLRS---DGLNGTTV 302

Query: 1504 SDNLAVQNKGFSFNAS-----GLF-EIHGATV-----VPIVSV--LAPEKLS 1543
DN + + GS N S GL AT+ +P + V L +K +
Sbjct: 303 -DNFSHLSALGSGDNRSSGGKERERGENGLSTSASNATIKNNYSQLPNLQVTLTHDKPT 361

Query: 1544 ASTRRRYETQVQTRLQTSANLHQSSEIEILAVDLPKETI 1584
A+ +RR E QV ++ ++L+ +K + + +L V+LP +
Sbjct: 362 ANYKRRLENQVAQQMSSTLSQFLKKETFV-VLVVELPPAVV 401

Score = 150 (57.9 bits), Expect = 4.2e-07, P = 4.2e-07
Identities = 66/300 (22%), Positives = 137/300 (45%)

Query: 1368 VPTAIGVSIADKISAAVLNMEESVTISSCDLLVSVGQMSMSRAINLTQKL-WTAGITA 1426
V + G++ ++DK+ AAV +E + + D+ + G + + +L W+ GI
Sbjct: 173 VLSGAGLTFSLDKLVAAV-GVEYAKDCRAIDVGICVCGTRPPLKDVYIMRLLWSVGIRC 231

Query: 1427 EIMYDWSQSQEELQEYCRHHEITYVALVSDKEGSHVKVSFEK--ERQTEKRVLETELVD 1484
I+ S+ +E Q+ R + +V LV++ V+ E+ ER + L E +
Sbjct: 232 GIVEAASELGDEAQLARLQAL-HVILVAENGLRVRSFERERFQERHLTRTEL-VEFIQ 289

Query: 1485 HVLQK--LRTKVTDERNGREA---SDNLAV-----QNLKGSFSFNASGLFEIHGATVVPI 1533
+L+ L D + A DN + + G ++AS + + +P
Sbjct: 290 KMLRSDDLNGTTVDNFSHLSALGSGDNRSSGGKERERGENGLSTSASNATIKNNYSQLPN 349

Query: 1534 VSV--LAPEKLSASTRRRYETQVQTRLQTSANLHQSSEIEILAVDLPKETILQFLSL- 1590
+ V L +K +A+ +RR E QV ++ ++L+ +K + + +L V+LP + +
Sbjct: 350 LQVTLTHDKPTANYKRRLENQVAQQMSSTLSQFLKKETFV-VLVVELPPAVVNAIVGAI 408

Query: 1591 -EWDADQAFNTTVKQLLSRLPK-QRYLKLVCDEIYNIKVEKKVSVLFLYSYRDDYYRIL 1648
+ ++ + ++ R K +RY+ + +E+ + + K ++ LYS D YR++
Sbjct: 409 NPRIKRETEPEINVIYERFSKYKRYISEINEEVVDYLSDAKTPIVALYSISDSYYRVI 468

View Prodom 2305

2305 p99.2 (23) SYH(12) // SYNTHETASE AMINOACYL-TRNA HISTIDYL-TRNA PROTEIN
LIGASE ATP-BINDING BIOSYNTHESIS HISTIDINE--TRNA HISRS KINASE
Length = 145

Score = 137 (53.3 bits), Expect = 3.9e-08, P = 3.9e-08
Identities = 41/131 (31%), Positives = 62/131 (47%)

Query: 1106 DHSGMLVMLPFDLRIPFARYVARNNI---LNLKRYCIERVFRPRK--LDRFHPKELLEC 1159
D G L+ L +DL +PFARYVA N + L LKRY I +V+R + + R +E +C
Sbjct: 18 DQGGELLSRLYDLTPFARYVAMNLLKVTNPLKRYHIAKVYRRDRPAMTRGRYREFYQC 77

Query: 1160 AFDIVTSTNSFLPXXXXXXXXXXXXQEFPALQERNYSIYLNHTMLLKAILLHCGIPEDK 1219
FDI+ ++ P + + N+ I +NH +L ++L P K
Sbjct: 78 DFDII-GEYDTMAPDAEILKILTEILSQLGIRELGNFKIKINHRGILDSSLQ----PWPK 132

Query: 1220 LSQVYIILYDA 1230
Q Y+ Y A
Sbjct: 133 TLQEYLTQYKA 143

View Prodom 1

>1 p99.2 (2773) CC2(14) KKIT(14) KPC1(13) // KINASE PROTEIN TRANSFERASE
ATP-BINDING SERINE/THREONINE-PROTEIN PHOSPHORYLATION RECEPTOR
TYROSINE-PROTEIN PRECURSOR TRANSMEMBRANE
Length = 431

FIG. 71

Score = 107 (42.7 bits), Expect = 0.0032, Sum P(2) = 0.0032
Identities = 36/106 (33%), Positives = 50/106 (47%)

Query: 848 DLKPVNIFLSDSDH-----VK-IGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG 900
DLKP NI LD + H +K I DFGLA + +S+ S ++ + +
Sbjct: 220 DLKPENILLDEESHENTPNMIKLIADFLAKE--IYSSSSTYEEMSSSQAVFGSHQTTST 277

Query: 901 MVGTALYVS-----PEVQGSTKSA-----YNQKVDLFSLGIIFFEM 936
M GT YVS PE SA Y+ K D++S G+I +EM
Sbjct: 278 MCGTPYYVSMKMAPEYMAPESSATNYQKYSTKSDVWSFGVILYEM 323

Score = 105 (42.0 bits), Expect = 3.5e-05, Sum P(3) = 3.5e-05
Identities = 35/102 (34%), Positives = 48/102 (47%)

Query: 824 RLWRLFREILDGLAYIHEK-----GMIHR----DLKPVNIFLSDSDH-----VK-IGDF 867
+L +I GL Y+H K +G+IHR DLKP NI LD + H +K I DF
Sbjct: 187 QLMHYVHQIAKGLEYLHKNQKHQGIHRAKKVDLKPENILLDEESHENTPNMIKLIAD 246

Query: 868 GLATDHLAFSADSKQDDQTGDLIKSDPSGHLTGMVGTALYVS 909
GLA + +S+ S ++ + + M GT YVS
Sbjct: 247 GLAKE--IYSSSSTYEEMSSSQAVFGSHQTTSTMCGTPYYVS 286

Score = 74 (31.1 bits), Expect = 0.91, Sum P(2) = 0.60
Identities = 30/127 (23%), Positives = 60/127 (47%)

Query: 341 QGTETEFNSLVKLSHPNVVRYLAMNKEQDDSIIVDIL-VEHISGVSLAAHLSHSGPIPV 399
+G+ E+ + + ++ L++ + +++ + + H+S S + LSHS
Sbjct: 134 EGSLEVEYMEYSGGSEDYMKKLSLETVMKIAMMILQFMQIMHMSSESES--LSHS----- 186

Query: 400 HQLRRYTAQLLSGLDYLSNS-----VVHKV----LSASNVLVDAEG-----TVK-ITD 443
QL Y Q+ GL+YLHS + ++H+ L N+L+D E +K I D
Sbjct: 187 -QLMHYVHQIAKGLEYLHKNQKHQGIHRAKKVDLKPENILLDEESHENTPNMIKLIAD 245

Query: 444 YSISKRL 450
+ ++K +
Sbjct: 246 FGLAKEI 252

Score = 65 (27.9 bits), Expect = 3.5e-05, Sum P(3) = 3.5e-05
Identities = 29/124 (23%), Positives = 50/124 (40%)

Query: 907 YVSPEVQGSTKSAYNQVDLFSLGIIFFEM-SYHPMVTASERIFVLNQLRDPTSPKFPED 965
Y++PE + Y+ K D++S G+I +EM + P E +++ S K E
Sbjct: 294 YMAPESSATNYQKYSTKSDVWSFGVILYEMLTGKPPFFPGES--EVSEEPYQSMKNMEV 351

Query: 966 FDDGEHAKQKSVISWLLNHDPAKRPT-----ATELLKSELLPPPMQMEESSELHE 1013
+ G + V+S ++ + P A +LLK L P+ E
Sbjct: 352 LEMGPREETIQKVMKIVEKKGERMPQPSSSNCPEVSQEAKDLLKKCLQKDPEKRRPTFEE 411

Query: 1014 VLHH 1017
+L H
Sbjct: 412 ILQH 415

Score = 55 (24.4 bits), Expect = 3.5e-05, Sum P(3) = 3.5e-05
Identities = 12/23 (52%), Positives = 18/23 (78%)

Query: 589 EFEELQ-LLGKGAFGAVIKVQNK 610
++E L+ LLGKG+FG V K ++K
Sbjct: 33 QYELLKKLLGKGSFGKVYKAKHK 55

Score = 49 (22.3 bits), Expect = 34., Sum P(2) = 1.0
Identities = 12/39 (30%), Positives = 24/39 (61%)

Query: 507 DLPADFQDFLKKCVCLD-DKERWSPQQLKHS-FINPQP 543
++ + +D LKKC+ D +K R + +++L+H F+ P
Sbjct: 385 EVSQEAKDLLKKCLQKDPEKRRPTFEEILQHPWFLMRNP 423

Score = 40 (19.1 bits), Expect = 0.0010, Sum P(3) = 0.0010
Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 596 LGKGAFGAVIK 606
LG G+FGAV K
Sbjct: 2 LGTGSFGAVYK 12

View Prodom 150228

>150228 p99.2 (1) O74297_NEUCR // CPC3 PROTEIN
Length = 108

FIG. 7m

<http://tango.mpi.com/seqanal/orfanal/14790.16890.html>

Score = 90 (36.7 bits), Expect = 0.0039, P = 0.0039
Identities = 32/105 (30%), Positives = 43/105 (40%)

Query: 1105 MDHSGMLVLPFDLRIPFARYVAR--NNILNLKRYCIERVFRPKLDRFHPKELLECAFD 1162
+D +G ++ LPFDL + AR +AR N+ + K Y +FR R P E FD
Sbjct: 3 LDQNGTVLQLPFDLMMGHARSLARITNSPVVQKYSFGNIFRDRH-GGGQPDVYGEVDVD 61

Query: 1163 IVTSTNSF-LPXXXXXXXXXXQEFPAQERNYSIYLNHTMLL 1206
IVTS L FP + L H+ LL
Sbjct: 62 IVTSDALDLALKEAEVIKVLDEIATAFPTVSSTPICFQLGHSDLL 106

View Prodom 137719

>137719 p99.2 (1) 074297_NEUCR // CPC3 PROTEIN
Length = 304

Score = 87 (35.7 bits), Expect = 0.61, Sum P(2) = 0.45
Identities = 41/156 (26%), Positives = 64/156 (41%)

Query: 19 YPQRQDHELQALEAIYGADFDLRPDACGPVKEPPEINLVLPQGLTGEEVYVKVLDLRVK 78
Y + Q+ E+ L+AIYG DF K P ++ + P + +E+ V L V
Sbjct: 44 YQEVQSESEVMVLQAIYGEDFTQHEAAHGAWQKSEPRFDIKIKPS--SDQEL--SVTLGVV 99

Query: 79 CPPTYPDVVPEIELKNAKGLSNESVNLKSRLEELAKK---HCGEVMIFELAYHVQSFLS 135
TYP P + +K+ L ES + E K + MI ++ ++ L
Sbjct: 100 MVATYPKTPPLLTIKDDHSL-RESTKFQKQFVETQPKIYAQAEQEMIDQIVEGIRDILE 158

Query: 136 E--HNK-----PP---PKSFHEEMLERRAQEEQQR 160
E K P ++ HE L R AQ E++R
Sbjct: 159 EAAQKKVQGLEIPSLEEERAAHEALARLAQSEKER 194

Score = 49 (22.3 bits), Expect = 0.61, Sum P(2) = 0.45
Identities = 13/48 (27%), Positives = 27/48 (56%)

Query: 1458 EGSHVKVKSFEKERQTEKRVLETVDHVLQK-LRTKVTDERNGREAS 1504
E ++ EKER+ K++ E++ + VL+ L+ ++ +RN + S
Sbjct: 181 EAELARLAQSEKEREERKKLEESKEEERVLEDMLQEELKRQRNKAKES 228

Score = 47 (21.6 bits), Expect = 0.96, Sum P(2) = 0.62
Identities = 15/61 (24%), Positives = 26/61 (42%)

Query: 238 KHRANSSGRSRERQYVCSNEDSPGSC-EILYFNMGSPDQLMVHKGKICGSDEQLGKLV 296
+++A S + R Q S + PG E L F+ P ++ G + +GK V
Sbjct: 222 RNKAKESRKKNRSHQLSPDRAPQDPGETDETLMPDQ--PCKITDGSNALFFQTIVIGKTV 279

Query: 297 Y 297
+
Sbjct: 280 F 280

Score = 47 (21.6 bits), Expect = 0.96, Sum P(2) = 0.62
Identities = 19/83 (22%), Positives = 33/83 (39%)

Query: 750 LPASDSSEDIIFDNEDENSKSQ-NQDEDCNEKNGCHESEPSVTTEAVHYLIQMEYCEKS 808
L S E ++ D E K Q N+ ++ +KN H+ P + + + +
Sbjct: 200 LEESKEEERVLEDMLQEELKRQRNKAKESRKKNRSHQLSPDRAPQDPGETDETLMPDQPC 259

Query: 809 TLRDTIDQGLYRDTVRLWRLPRE 831
+ D L+ TV +FRE
Sbjct: 260 KITDGSNALFFQTIVIGKTVFRE 282

FIG. 7n

14790 Expression in HBV+ Livers

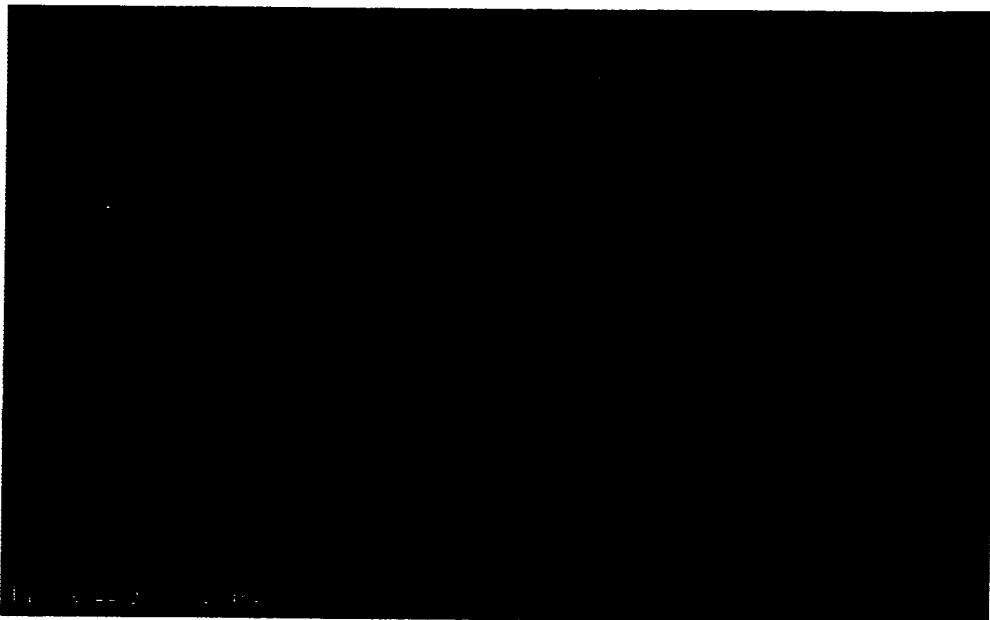


FIG. 8a

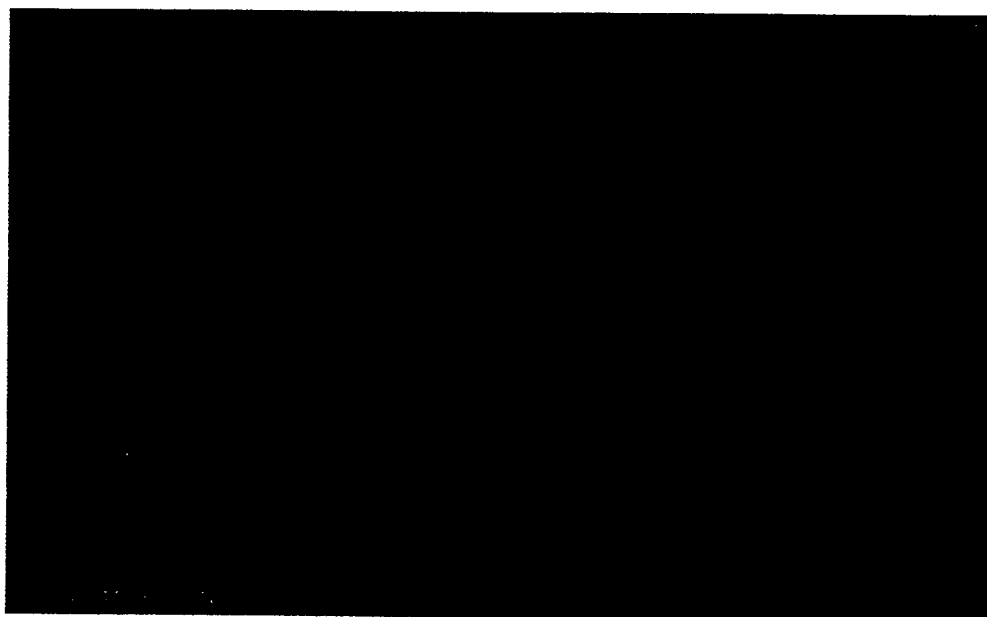


FIG. 8b

00515806-022900

FIG. 9a

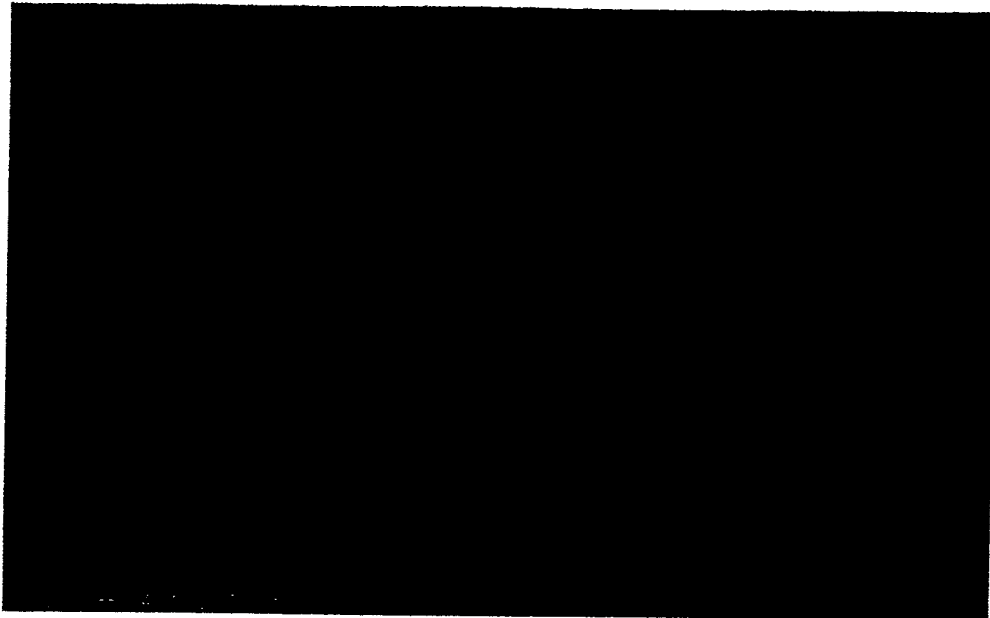


FIG. 9b

